

FIGURE 1

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somGD A MSHPTSTVSEPSN-LDFQVPLKGNFVNLNSLHGNNNSNGYSSFSNSVHFGGLAT----QN 5
csMGD A MRNPSTV/QENGSS-VSCFISGLQYFAFSRFLNLNSGCGSSSHSLYLNGFNRYRCVK 59
acMGD A MQNPSTV/QESAAVDFDFPRLRLGLTSRNRSPCSNSDGYALSSSNALYNGFRTLPS-RR 59
acMGD B ..... 0

somGD A RYKFVNSLSF---SKGGSNLKRIISDFNRVIRLHCORI-PLGFSSTGLN--SGESNGVSD 109
csMGD A PPRSGLASLSL--SRGSSSLRRFVNEFNNVKIFHCCHKP-PLGFASLGGV--SDSTENGR 114
acMGD A MGKTLASLSFNTKSSAGGSLRRFISDFNSFVIFHCOKVVPSPASVGGVGLSSDENGIRE 119
acMGD B ----MATTVN---ALAKYLERVVTQSKSVFVTSDDGEKTHRHTHHHRIRKSYDDIDE 53
.....

somGD A NGHG-VLEDVRVPVNAVEPESPKRVILILMSDTGGGHRASAEAIKAAFNEEPGDDYQVFT 168
csMGD A DQFG-VSQDGLPLNKIEAENPKRVILILMSDTGGGHRASAEAIKAAFNEEPGDMYQVFT 173
acMGD A NGTGGVGLGEGGLPLNGVEADPKRVILILMSDTGGGHRASAEAIKAAFNEEPGDDYQVFT 179
acMGD B DESS-----LELIQIGAERTKQVILILMSDTGGGHRASAEAIRDAFKISFGDKYRVTVK 155
.....

n1
somGD A DQWSEHTPWPFPNQLPRSYNFLVKHGPLKMMYYGTSPRVINQSNFAATSTFFIAREVARGL 128
csMGD A DLWTEHTPWPFPNQLPRSYNFLVKHGTLWNGTYVYVAPKVIHQSNFAATSTFFIAREVARGL 213
acMGD A DLWTDHTPWPFPNQLPRSYNFLVKHGTLWNGTYVGTSPRVINQSNFAATSTFFIAREIAQGL 239
acMGD B DVNKEYTGWPLNDMERSYKFMVGVQVQWKVAFHSTSPKWIHSCYLAALAAAYYAKEVEAGL 166
.....

n2
somGD A MKYQPDIIISVHPLMQHVPLRLILAGRGLEKIVFTVITDLSCTHPTWFHKLVTRCYCPS 298
csMGD A MKYRPDIISVHPLMQHVPLRLILRAGGLKLNKIVFTVITDLSCTHPTWFHKLVTRCYCPS 291
acMGD A MKYQPDIIISVHPLMQHVPLRLVLRSGLLKKIVFTVITDLSCTHPTWFHKLVTRCYCPS 299
acMGD B MEYKPEIISVHPLMQHILPLWLKQWELQKRVLEVTVITDLSCTHPTWFHGPVNRRCYCPS 226
.....

somGD A NEVAKRATKAGLOPSQIKYVGLPVRPSPFVRSVRPKNELRKELGMDENLPAVLLMGGGEGM 148
csMGD A TEVAKRALTAGLQPSKLYVGLPVRPSPFVKPIRPKIELRKELGMDENLPAVLLMGGGEGM 153
acMGD A TEVAKRAQKAGLETSSQIKYVGLPVRPSPFVKPVRPKVELRRELGMDENLPAVLLMGGGEGM 159
acMGD B QEVAKRALFDGLESGQVRVGLPVRPSPFARAVLVKDLRRELGMDDLRVLLMGGGEGM 286
.....

n3* n4
somGD A GPTEATARALGNALYDANLGEPTQGLLVIICGRNKGLAGLSSIDWKIPVQVKGFVTIKEE 408
csMGD A GPTEATAKALSALYDENGGEPTQGLVVICGRNKGLAGRLSIDWKIVBQVKGFVTIKEE 413
acMGD A GPTEATARALADALYDKNLEAVGQVLIIICGRNKGLQGLSSIDWKIPVQVKGFVTIKEE 419
acMGD B GPVKETAKALEEFLYDKNRKPITGQMVVVICGRNKGLASALBIDWKIPVKVGFPTQHEK 145
.....

n5
somGD A CMGACDCIITKAGPGTIAEAMIRGLPIILNDYIAGQEAGNVPYVYVENGIGRYLKSPEKIA 458
csMGD A CMGACDCIITKAGPGTIAEAMIRGLPIILNDYIAGQEAGNVPYVYVENGCGKFSKSPKIEA 471
acMGD A CMGACDCIITKAGPGTIAEAMIRGLPIILNDYIAGQEAGNVPYVYVENGCGKFSKSPKIE 479
acMGD B WMGACDCIITKAGPGTIAESLIRSLPIILNDYIPGQEKQVVPYVYVENGAGVFRSPKETA 406
.....

n6
somGD A KTVSQWFGPKANELOIMSONALKHARPDPAVFKIVHDLDELVRQKIFVRQYSCAA----- 522
csMGD A NIVAKWFGPKADELIMSONALRLARPDAVFKIVHDLDELVRQKISFPQYSG----- 525
acMGD A KIVADWFGPKAKEIMSONALRLAKPEAVFKIVHDMDELVRKINSLPQLSCTA----- 531
acMGD B RIVGEWFSFTKDELEQTSNARKLAQPEAVFDIVKIDELSEQRGPLASVSNLTSSFSASLV 468
.....

h7*

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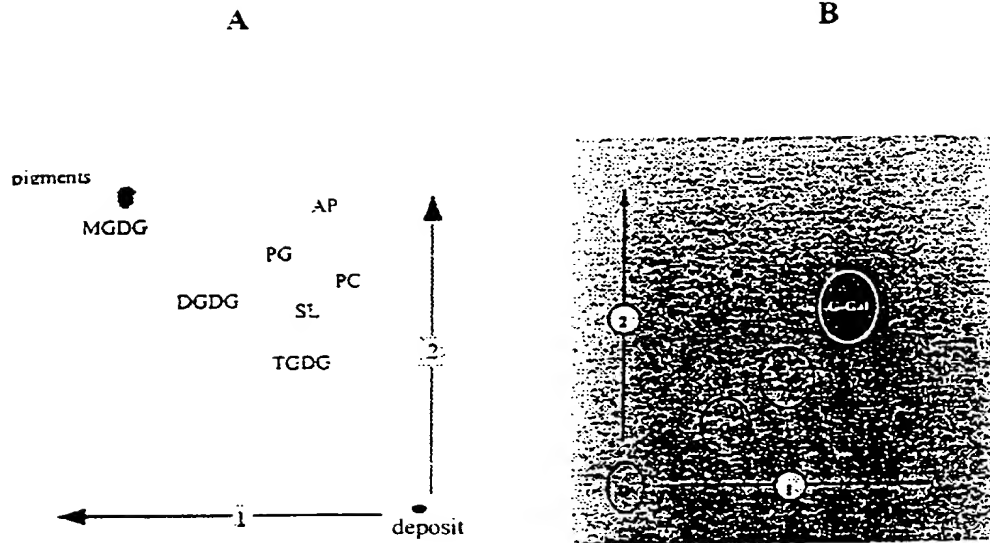
B

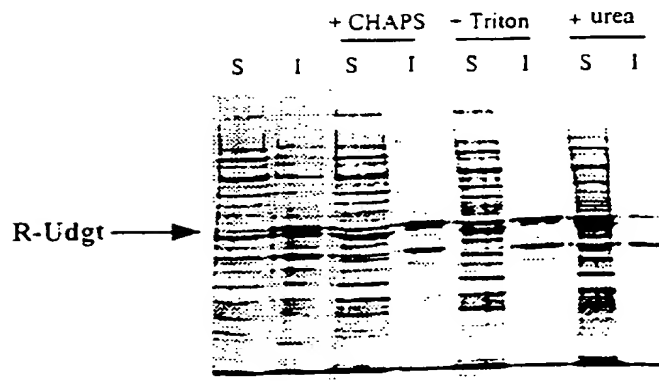
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1	50MGD	A
2	50MGD	A
3	50MGD	A
4	50MGD	B

FIGURE 2

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**FIGURE 3**

FIGURE 4

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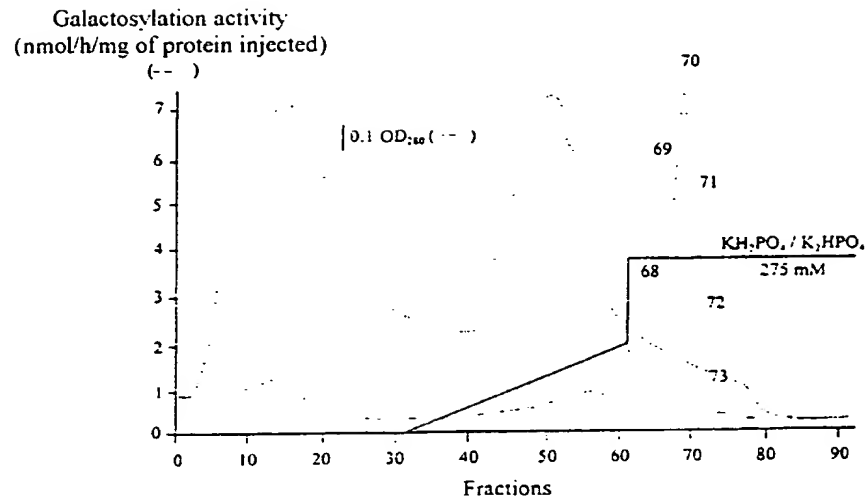


FIGURE 5A

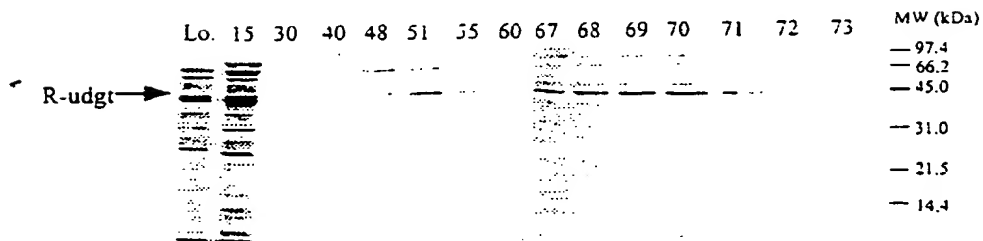


FIGURE 5B